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1 1
GTCTTCCACCATGCACTCGCTGGCTTCTTCTGTGGCGTGTCTCTGTCTCGCCGCTG
-----+-----+-----+-----+-----+-----+-----+
CAGGAAGGTGTAGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGGCGAC
M H S L G F F S V A C S L L A A A
60
CGCTGCTCCCGGGTCTCTCGGAGGGCGCCCGCGCGCGCGCGCTTCGAGTCCGGAATCG
-----+-----+-----+-----+-----+-----+-----+
GCGACGAGGGCCAGGAGCGCTCCGCGGGCGGCGGCGGCGGAAGCTCAGGCCCTGAGC
L L P G P R E A P A A A A A A F E S G L D
120
ACCTCTCGGACGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG
-----+-----+-----+-----+-----+-----+-----+
TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC
L S D A E P D A G E A T A Y A S K D L E
180
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAATCACTGACTGTACTTACCCAGAAT
-----+-----+-----+-----+-----+-----+-----+
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
E Q L R S V S S V D E L M T V L Y P E Y
240
ATTGGAAAATGTACAAGTGTCAAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
-----+-----+-----+-----+-----+-----+-----+
TAACCTTTTACATGTTACAGTCGATTCCCTTTCCTCCGACCGTGTATGTCTCTTGTC
W K M Y K C Q L R K G G W Q H N R E Q A
300
CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTGCTGCAGCACATTATAATACAG
-----+-----+-----+-----+-----+-----+-----+
GGTTGGAGTTGAGTTCCTGTTCTCTGTGATATTTAAACGACGTCGTGTAATATATGTC
N L N S R T E E T I K F A A A H Y N T E
360

FIG. 1A



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361 AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
-----+-----+-----+-----+-----+-----+-----+
TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
I L K S I D N E W R K T Q C M P R E V C

420

421 GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
-----+-----+-----+-----+-----+-----+-----+
CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
I D V G K E F G V A T N T F F K P P C V

480

481 TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGGTGCAGTGCATGAACACCA
-----+-----+-----+-----+-----+-----+-----+
ACAGGCAGATGTCTACACCCCAACGACGTTATCACTCCCGACGTCACGTACTTGTGGT
S V Y R C G G C C N S E G L Q C M N T S

540

541 GCACGAGCTACCTCAGCAAGACGTTATTGAAATTACAGTGCCTCTCTCTCAAGGCCCA
-----+-----+-----+-----+-----+-----+-----+
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTACGGAGAGAGAGTTCCGGGGT
T S Y L S K T L F E I T V P L S Q G P K

600

601 AACCAAGTAACAATCAGTTTGGCCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
-----+-----+-----+-----+-----+-----+-----+
TTGGTCATTGTTAGTCAAACCGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC
P V T I S F A N H T S C R C M S K L D V

660

FIG. 1B



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661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACTACCACAGTGTC
-----+-----+-----+-----+-----+-----+-----+
AAATGTCCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG
Y R Q V H S I I R R S L P A T L P Q C Q
720

721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
-----+-----+-----+-----+-----+-----+-----+
TCCGTCGCTTGTTCGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCACGG
A A N K T C P T N Y M N N H I C R C L
780

781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
-----+-----+-----+-----+-----+-----+-----+
ACCGAGTCCTTCTAAATAACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
A Q E D F M F S S D A G D D S T D G F H
840

841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTGAGTGTGTCTGCAGAG
-----+-----+-----+-----+-----+-----+-----+
TACTGTAGACACCTGGTTGTTCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
D I C G P N K E L D E E T C Q C V C R A
900

901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAAACTCATGCCAGT
-----+-----+-----+-----+-----+-----+-----+
GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA
G L R P A S C G P H K E L D R N S C Q C
960

FIG. 1C



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961	GTGTCTGTAAAAAACAACCTCTTCCCGAGCCAATGTGGGCCAACCGAGAATTGTATGAAA -----+-----+-----+-----+-----+-----+-----+ CACAGACATTTTGTGTTGAGAAAGGGGTCCGGTTACACCCCGGTTGGCTCTTAAACTACTTT V C K N K L F P S Q C G A N R E F D E N	1020
1021	ACACATGCCAGTGTGTATGTAAAGAACCTGCCCGACAGAAATCAACCCCTAAATCCTGGAA -----+-----+-----+-----+-----+-----+-----+ TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT T C Q C V C K R T C P R N Q P L N P G K	1080
1081	AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC -----+-----+-----+-----+-----+-----+-----+ TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTCCCTTTCTTCAAGG C A C E C T E S P Q K C L L K G K K F H	1140
1141	ACCACCAAACATGCAGCTGTTACAGACGGCCCATGTACGAACCGCCAGAGGCTTGTGAGC -----+-----+-----+-----+-----+-----+-----+ TGGTGGTTGTACGTCGACAAATGTCTGCCGGTACATGTCTGGCGGTCTTCCGAAACACTCG H Q T C S C Y R R P C T N R Q K A C E P	1200
1201	CAGGATTTTCATATAGTGAAGAAAGTGTGTGTCGTTGTGTCCTTCATATTGGCAAGACCAC -----+-----+-----+-----+-----+-----+-----+ GTCCATAAAGTATACCTTCTTACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG G F S Y S E E V C R C V P S Y W Q R P Q	1260

FIG. 1D



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1261 AAATGAGCTAAGATTGTAAGTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
-----+-----+-----+-----+-----+-----+-----+
TTTACTCGATTCTAACAATGACAAAAAGGTCAAGTAGCTAAAAAGATAATACCTTTTGACACA
M S *
1320
1321 TGCCACAGTAGAACTGTCTGTGAACAGAGAGAGACCCTTGTGGTCCAATGCTAACAAAGACA
-----+-----+-----+-----+-----+-----+-----+
ACGGTGTCACTTTGACAGACACTTGTCTCTCTCTGGGAAACACCCAGGTACGATTGTTTCTGT
1380
1381 AAAGTCTGTCTTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
-----+-----+-----+-----+-----+-----+-----+
TTTCAGACAGAAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC
1440
1441 CAAAAGGCCTCTGTAAAGACTGGTTTCTGCCAATGACCAAAACAGCCAAGATTTTCCTC
-----+-----+-----+-----+-----+-----+-----+
GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCTGGTTCTAAAGGAG
1500
1501 TTGTGATTTCTTTAAAGAAATGACTATATAATTTATTTCCACTAAAAATATTTGTTTCTGC
-----+-----+-----+-----+-----+-----+-----+
AACACTAAAGAAAATTTTCTTACTGATATATAATAAAGGTGATTTTATAACAAAGACG
1560
1561 ATTCATTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTATATCAT
-----+-----+-----+-----+-----+-----+-----+
TAAGTAAAAATATCGTTGTTGTTAAACCATTTTGAGTGACACTAGTTATAAAAAATATAGTA
1620
1621 GCAAAAATATGTTTAAAAATAAAATGAAAATGTAATTTATAAAAAA
-----+-----+-----+-----+-----+-----+-----+
CGTTTTTATACAAAATTTTATTTTACTTTTAAACATAAAATATTTT
1674

FIG. 1E



1 CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
-----+-----+-----+-----+-----+-----+-----+
61 AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAAATGTACAAGTGTCAAGCTAAG
-----+-----+-----+-----+-----+-----+-----+
M T V L Y P E Y W K M Y K C Q L R
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAGAC
-----+-----+-----+-----+-----+-----+-----+
K G G W Q H N R E Q A N L N S R T E E T
181 TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
-----+-----+-----+-----+-----+-----+-----+
I K F A A A H Y N T E I L K S I D N E W
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTATAGATGTGGGGAAGGAGTTTGGAGT
-----+-----+-----+-----+-----+-----+-----+
R K T Q C M P R E V C I D V G K E F G V
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCTACAGATGTGGGGTTGCTG
-----+-----+-----+-----+-----+-----+-----+
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

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361 CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCAGCAGCTACCTCAGCAAGACGTTATT
N S E G L Q C M N T S T S Y L S K T L F
421 TGAATTACAGTGCCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTGGCCAATCA
E I T V P L S Q G P K P V T I S F A N H
481 CACTTCCTGCCGATGCATGTCTAACTGGATGTTTACAGACAAAGTTCATTCCATTATTAG
T S C R C M S K L D V Y R Q V H S I I R
541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCTCAGGCAGCGAACAAGACCTGCCCCCACC
R S L P A T L P Q C Q A A N K T C P T N
601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTTCCTC
Y M W N N H I C R C L A Q E D F M F S S
661 GGATGCTGGAGATGACTCAACAGATGGATTCCATCATCTGTGGACCAACAAGGAGCT
D A G D D S T D G F H D I C G P N K E L

FIG. 2B





721 GGATGAAGAGACCTGTCTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
D E E T C Q C V C R A G L R P A S C G P

781 CCACAAAGAACTAGACAGAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCCAG
H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTGGGCCAACCGAGAATTGATGAAACACATGCCAGTGTGTATGTAAGAAGAAC
Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTAAAGGAAAGAAAGTTCCACCACCAACATGCAGCTGTTACAGACG
Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAAGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
P C T N R Q K A C E P G F S Y S E E V C

FIG. 2C



1081
TCGTTGTGTCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCTCA
- - - - -
R C V P S Y W Q R P Q M S *
- - - - -

1141
GTTTCATCGATTTTCTATTATGGAAAACTGTGTGGCCACAGTAGAACTGTCTGTGAACAGA
- - - - -

1201
GAGACCCCTTGTGGTCCATGCTAACAAAGACAAAGTCTGTCTTTTCCTGAACCATGTGGA
- - - - -

1261
TAACTTTACAGAAATGGACTGGAGCTCATCTGC AAAAGGCCCTCTTGTAAAGACTGGTTT
- - - - -

1321
CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAGAAATGACTATA
- - - - -

1381
TAAATTTATTTCCACTAAAAATATTGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
- - - - -

1441
AAAACCTCACTGTGATCAATATTTTATATCATGCAAAATATGTTTAAAAATAAAATGAAAA
- - - - -

1501
TTGTATTATAAAAAAAAAAAAA
- - - - -

FIG. 2D



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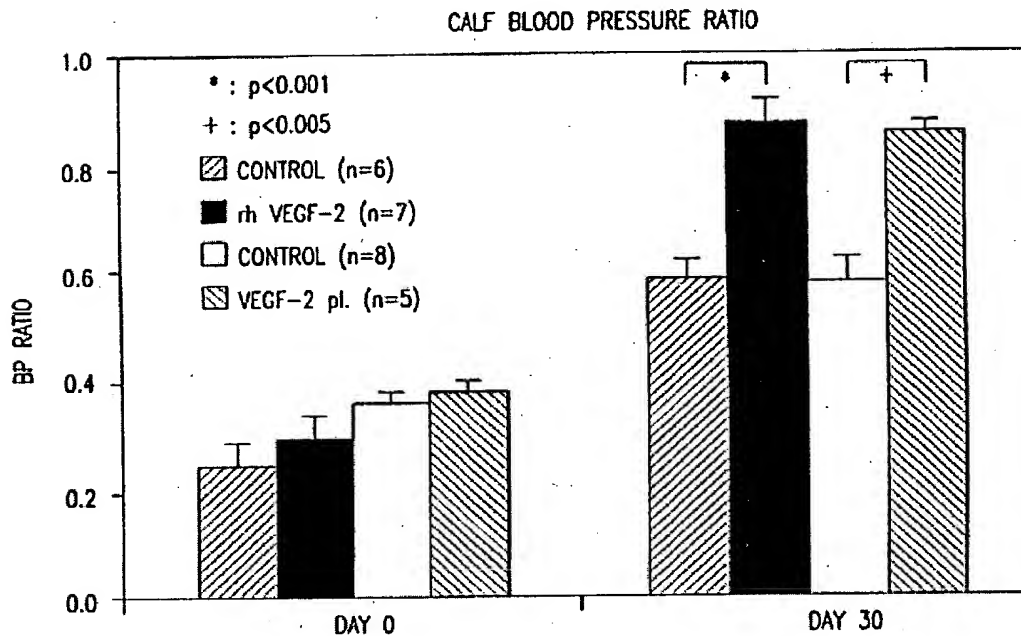


FIG. 25C

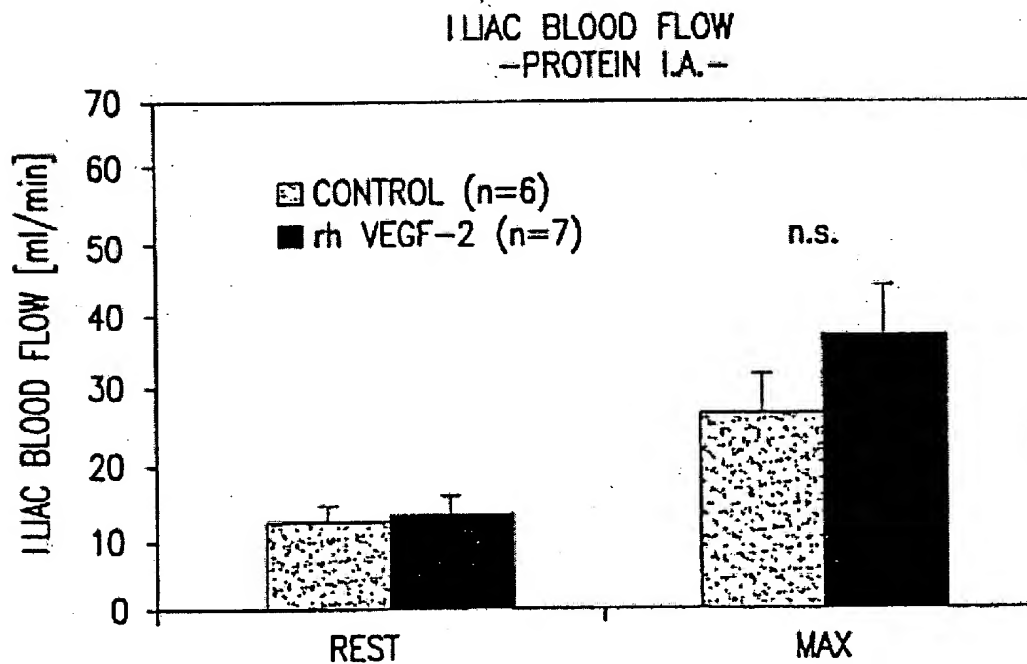
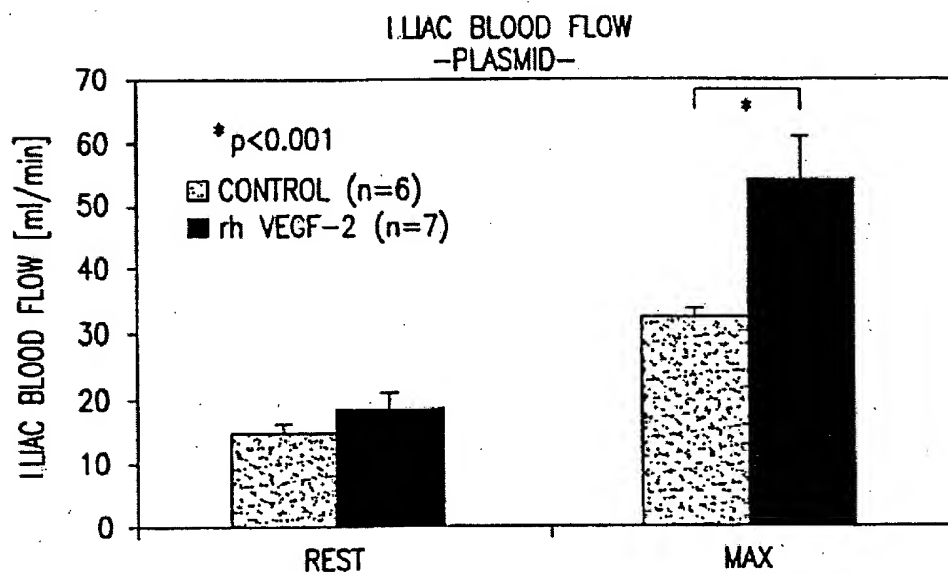
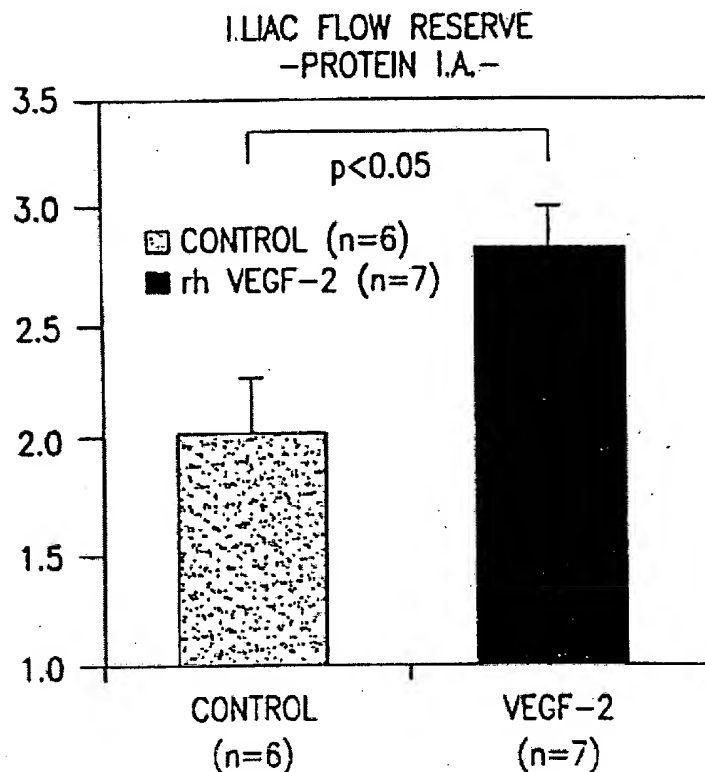


FIG. 25D



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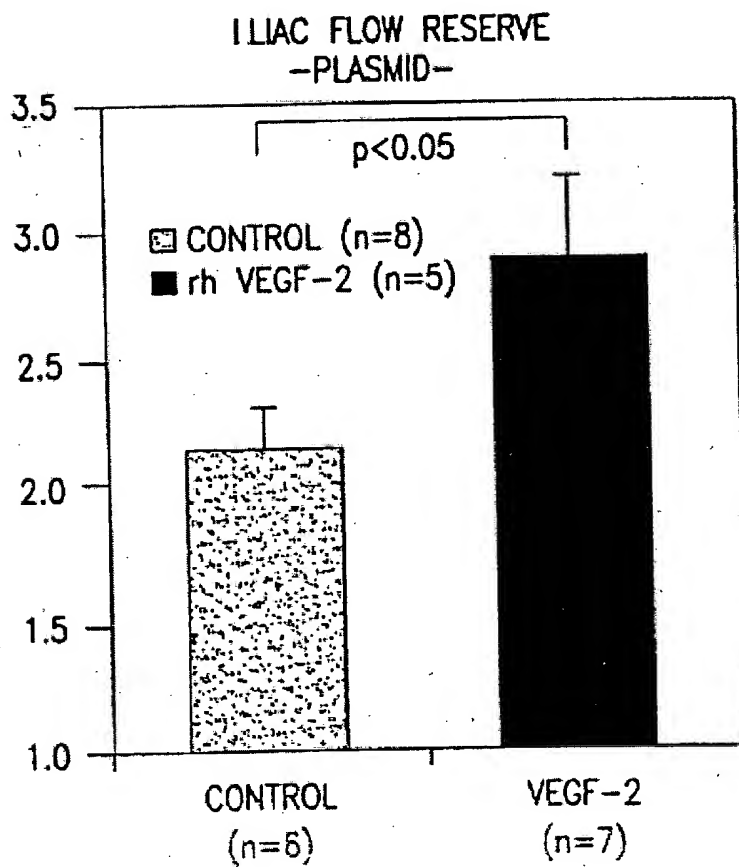


FIG. 25G

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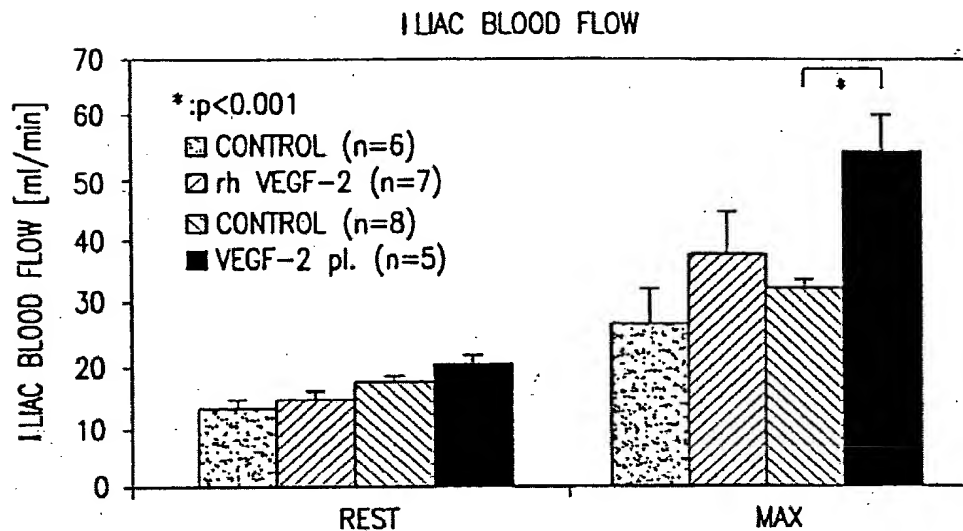


FIG. 25H

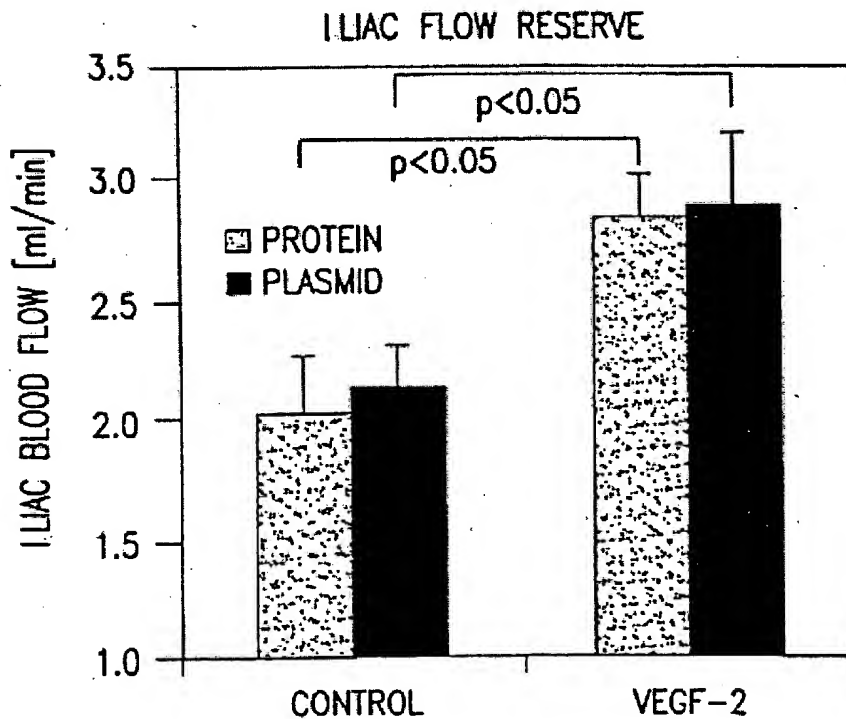


FIG. 25I